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First Genetic Study of Bed Bugs Reveals Possible Pesticide-Resistance Genes

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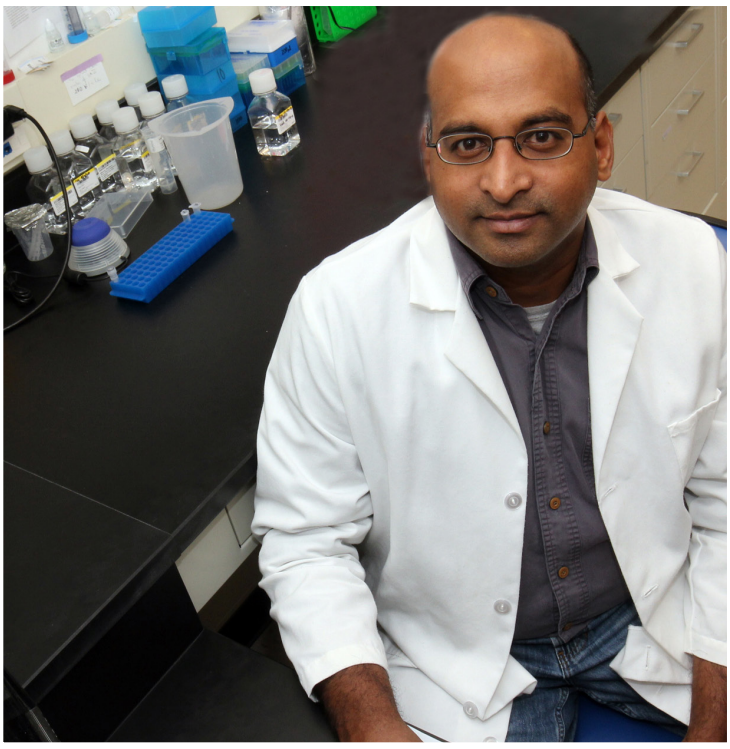
Background

As a result of the widespread use of DDT and other long-lasting residual insecticides, bed bugs (*Cimex lectularius*) have been considered a minor nuisance since World War II. Bed bug numbers have increased in the past decade as much as 500 percent in North America and other parts of the world—costing billions of dollars to homeowners and businesses annually and requiring the use of large quantities of pesticides, many of which are ineffective.

Reasons behind the spike in bed bug infestations include a boom in international travel; an increased exchange of used furniture; a shift from powerful but dangerous insecticides, such as DDT, to more selective control tactics; and the development of resistance among bed bug populations to currently used pesticides.

The common assumption today is that pesticide resistance in bed bugs results from point mutations in certain genes. However, the role of certain enzymes in the pesticide resistance of bed bugs is poorly understood. Specific enzymes have been shown in other insects to act as detoxification agents, allowing the insects to get rid of toxic compounds such as insecticides, and not be killed by them. Our study looked closely at those groups of enzymes in bed bugs.



Objectives

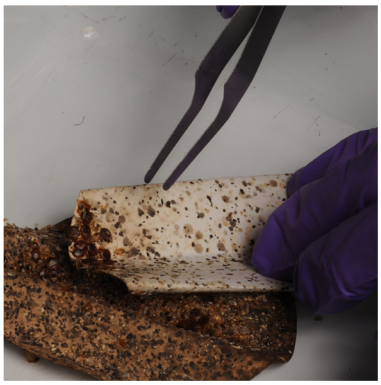
This research aimed to be the first study to elucidate the genetic makeup of the bed bug, and to obtain fundamental molecular knowledge regarding potential defense pathways and genes that may be involved in resistance to commonly used pesticides.

For the study, scientists analyzed both laboratory-reared bed bugs susceptible to insecticides, and pesticide-exposed bed bugs collected from a Columbus, Ohio, apartment in 2009 and 2010. This analysis led to the identification of 35,646 expressed sequence tags, or ESTs, which are instrumental in gene discovery and sequencing work. Before this study was conducted, less than 2,000 ESTs for bed bugs had been filed in the National Center for Biotechnology Information (NCBI) databases. This information alone is expected to advance additional genetic studies of bed bugs and comparative molecular analyses of blood-feeding insects.

Impacts

From the database we created, we profiled the transcript level for certain genes in different developmental stages (early-stage nymphs, late-stage nymphs, and adults) of pesticide-susceptible and pesticide-exposed bed bugs.

The insecticides being used right now are based on the idea that resistance in bed bugs is caused by point mutations in genes, but we are finding out that the mode of resistance could be attributed to a combination of changes in the bugs' genetic makeup (such as mutations) as well as transcriptomic adjustments leading to differential gene expression. Pinpointing such defense mechanisms and the associated genes could lead to the development of novel methods of control that are more effective.



This research was the first major step in paving the road to the identification of potential genes associated with pesticide resistance. As a result of this research, potential new control methods for the troublesome bed bug—whose sudden resurgence in the United States has led to a public health scare and has cost the global economy billions of dollars—may be well within reach.

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